characterize membrane protein structures. However, most present membrane protein NMR structure determination approaches refine a protein structure in implicit solvent, and therefore do not provide detailed protein-lipid/detergent interactions, which are essential in determining the relative orientation in the protein's helical domains that is related to its function. In addition, membrane protein NMR observables are often insufficient to clearly define all the side chain-side chain interactions. These undefined interactions could be critical in the protein's structure and function. To overcome these limitations, various NMR observables were utilized as restraints for molecular dynamics (MD) simulations in the explicit (bilayer and micelles) membranes. With various NMR restraint (CSA, DC, NOE and RDC) potentials, we have investigated the orientation of Pf1 coat protein and DAP12-NKG2C complex. The former is a single-pass transmembrane helical protein with a membrane associated periplasmic helix, and the latter is a complex with undefined but functionally required polar side chain interactions. The resulting structures satisfy the NMR observables and compared to the published structures. With respect to the explicit membrane, the disposition of Pf1 TM helix was identified and the dynamic nature of the periplasmic helix orientation was observed. For DAP12-NKG2C complex, several functionally required polar residues adopted different side chain conformations to enhance the complex assembly.

2032-Pos Board B802
Finite Length Effects for Osmotic Pressures of PEG Polymers
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Previously we derived a one-parameter scaling-law equation of state for the osmotic pressures of polyethylene glycol (PEG) polymers in water, applicable over a broad range of polymer sizes and concentrations (*J. Phys. Chem. B*, 2009, 113, 3709). The derived equation is a non-virial linear combination of a low-concentration van't Hoff (vH) term and a higher-concentration des Cloizeaux (dC) term. A single parameter α locates the crossover from dilute vH to semidilute dC behavior. The value of α was determined by an empirical fit to the concentration-dependent data of Rand et al. (*loc.cit.*) for PEGs of molecular weights ranging from 300 to 20,000 daltons. Appropriate scaling collapsed all the data onto a single curve that was well fit by our equation of state with the single parameter $\alpha = 0.49 \pm 0.01$. Now, by fitting α to the scaled osmotic pressures of each polymer separately, we find a small but systematic dependence of α on polymer size. As the number of monomers N increases, $\alpha(N)$ decreases monotonically toward an asymptotic value that we call α^*. The interaction strength of shorter polymers is thus larger than that of longer polymers. Because scaling theories assume polymers of infinite length, α^* can be viewed as the value of α in the scaling limit. A correction-to-scaling formula derived from renormalization group theory provides an excellent fit to $\alpha(N)$ for PEG polymers, yielding $\alpha^* = 0.43 \pm 0.02$. The present formulation for $\alpha(N)$ further improves the accuracy of the osmotic pressures of PEG polymers calculated by our equation of state.

2033-Pos Board B803
Determining the Optimal Degree of Macromolecular Crowding in Solution Using Fluorescence Recovery after Photobleaching (FRAP)
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Macromolecular crowding (MMC) is a feature of cellular interiors and, in multicellular organisms, also of extracellular environments. Recreating this crowdedness via employment of macromolecules is a valuable tool in studying protein folding behaviour, supramolecular assembly, acceleration of biochemical reactions and extracellular matrix deposition. Optimal MMC in solution has been mostly determined empirically by quantitating biochemical endpoints (PCR product, amount of matrix deposited). Here, we sought to develop a technique allowing the direct observation of MMC in a purely physical manner in order to make predictions of optimal crowder concentrations. We have shown earlier by dynamic light scattering that above certain concentrations the hydrodynamic radii of Ficolls 70 and 400 shrink (Harve et al 2007). We described this event as self-crowding.
Here, we studied this phenomenon with FRAP in order to monitor changes in the molecular diffusion velocity of FITC-tagged Ficoll 70 and Ficoll 400. Both crowders are sucrose polymers, stable at neutral pH, and globular in shape.
FRAP allowed us to establish a clear link between molecular speed variation and degree of crowdedness. We verified that beyond a threshold concentration self-crowding occurred as evidenced by a speed increase for the molecules undergoing shrinking. Maximum compaction of Ficoll molecules was reached with increasing concentrations. Further concentration increases led to a rapid drop of diffusion velocity.
By purely physical means we can now define the optimal crowding concentration as the greatest possible concentration allowing for the greatest possible diffusion velocity. Interestingly enough, the determined values match those obtained from biological read-outs published earlier (Chen et al 2011) very well. This technique now opens up the possibility to determine for each potential macromolecule the crowding points rapidly, and to predict suitable concentrations for application in biological systems.

2034-Pos Board B804
The Role of Hydrodynamic Interactions in Self-Organization of Biological Molecules
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Self-organization is one of the most fundamental phenomena in biology. Elucidating the mechanisms of the self-assembly of biological molecules, such as protein folding/binding and formation of lipid bilayer membranes, have been a fascinating topic over decades in biological field. Hydrodynamic interactions (HIs) give rise to collective motions between molecules. Therefore, they may play an important role on dynamics of self-assembly. Although there are significant advances in theoretical and computational studies on thermodynamics and kinetics of self-assembling systems recent years, analysis on effects of HIs to the reactions are limited due to their high complexity. Here, by using a Brownian dynamics (BD) simulation technique, we evaluate the importance of HIs on kinetic of self-assembly in a set of examples, formation of lipid membrane and actin polymerization reaction. We first built coarse-grained models of lipid and actin monomer. A cluster of lipid molecules was represented by two particles, one is hydrophilic head group and the other is hydrophobic tail group, and attractive interaction between tail groups was applied. For actin polymerization system, each monomer was represented by two particles and an angle-dependent attractive interaction was applied to form long filaments. In BD simulations, the Rotne-Prager-Yamakawa tensor was used to account for HIs between particles. In the early stage of self-assembly, HIs between inter-monomer particles decelerated the association rate of monomers to form oligomers compared with that in the simulations without inter-monomer HIs in both systems. On the other hand, the HIs accelerate the reaction of oligomers to form a fully-assembled state or much longer polymers. This phenomenon could be explained by the Kirkwood-Riseman theory. Those results clearly suggest that HIs greatly affect kinetics of self-assembly reactions and considering the interactions is crucial for studying dynamics of biological systems.

2035-Pos Board B805
Efficient RDF Computation in Particle Simulations Data
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Analysis of large particle simulation data often involves computing Radial Distribution Function (RDF). A novel algorithm to compute RDF based on a data structure called ***density map*** (DM) is presented. DM is essentially a grid dividing simulated space into cells (3D cubes) of equal size (volume), which can be easily implemented by augmenting a Quad-tree index.
The algorithm first divides the simulated space into a DM, each cell of which records the number of data points in it. The DMs with different cell sizes have to be maintained; therefore, we organize all point coordinates into a point region Quad-tree. Then we build histogram of distances between all pairs of particles, required to compute RDF. Two cells A and B (with particle counts n_a and n_b) of a DM are said to be ***resolvable*** if the minimum and maximum distance between the two cells fall into a required distance range, which is represented by a bucket of the histogram. If two cells resolve into bucket k, the number of distances that fall into it is incremented by $n_a n_b$. The unresolved cell pairs can be handled in two different ways:
(1) Resolve all cell pairs of the children of A and B in the Quad-tree. If the cells are leaf nodes, then compute point-to-point distances to update the histogram. Entire tree is traversed while skipping sub-trees rooted at resolvable cells.
(2) Apply some heuristics, adding very small errors, to distribute the number of distances into buckets covered by the minimum and maximum distance between cells. It can be applied at any required level to stop traversing the tree further.
The RDF is computed by utilizing the histogram, which is straightforward. Thus, making one of the above choices controls the error and speed in RDF computation.